

SEQUENCE LISTING

<110> Syngenta
Jepson, Ian
Martinez, Alberto
Greenland, Andrew James

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<150> US 08/653,648
<151> 1996-05-24

<150> US 09/564,418
<151> 2000-05-03

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<170> PatentIn version 3.2

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 Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg Phe Leu Asn Glu
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 Lys Leu Met Glu Arg Thr Arg Leu Arg Asn Val Pro Pro Leu Thr Ala
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 Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly
 355 360 365

Ser Leu Ala Ser Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu
 370 375 380
 Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu
 385 390 395 400
 Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu
 405 410 415
 Thr Tyr Asn Gln Leu Ala Val Ile Thr Lys Leu Ile Trp Tyr Gln Asp
 420 425 430
 Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln
 435 440 445
 Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr
 450 455 460
 Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly
 465 470 475 480
 Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu
 485 490 495
 Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr
 500 505 510
 Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr
 515 520 525
 Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu
 530 535 540
 Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu
 545 550 555 560
 Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu
 565 570 575
 Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr
 580 585 590
 Leu Arg Ile Thr Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu
 595 600 605
 Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu
 610 615 620
 Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg
 625 630 635 640
 Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro
 645 650 655
 Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu Asp Glu Arg
 660 665 670
 Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr
 675 680 685
 Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala
 690 695 700
 Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu
 705 710 715 720
 Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln
 725 730 735

Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln
 740 745 750
 Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu
 755 760 765
 Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu
 770 775 780
 Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile
 785 790 795 800
 Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr
 805 810 815
 Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val
 820 825 830
 Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr
 835 840 845
 Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln Gln Gln Leu
 850 855 860
 Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr Ala
 865 870 875

<210> 9
 <211> 536
 <212> PRT
 <213> Chironomus tentans

<400> 9

Met Lys Thr Glu Asn Leu Ile Val Thr Thr Val Lys Val Glu Pro Leu
 1 5 10 15
 Asn Tyr Ala Ser Gln Ser Phe Gly Asp Asn Asn Ile Tyr Gly Gly Ala
 20 25 30
 Thr Lys Lys Gln Arg Leu Glu Ser Asp Glu Thr Met Asn His Asn Gln
 35 40 45
 Thr Asn Met Asn Leu Glu Ser Ser Asn Met Asn His Asn Thr Ile Ser
 50 55 60
 Gly Phe Ser Ser Pro Asp Val Asn Tyr Glu Ala Tyr Ser Pro Asn Ser
 65 70 75 80
 Lys Leu Asp Asp Gly Asn Met Ser Val His Met Gly Asp Gly Leu Asp
 85 90 95
 Gly Lys Lys Ser Ser Ser Lys Lys Gly Pro Val Pro Arg Gln Gln Glu
 100 105 110
 Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
 115 120 125
 Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
 130 135 140
 Lys Asn Ala Val Tyr Cys Cys Lys Phe Gly His Glu Cys Glu Met Asp
 145 150 155 160
 Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu
 165 170 175

Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala
 180 185 190
 Ile Lys Arg Lys Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Val Pro
 195 200 205
 Gly Ile Val Gly Ser Asn Thr Ser Ser Ser Ser Leu Leu Asn Gln Ser
 210 215 220
 Leu Asn Asn Gly Ser Leu Lys Asn Leu Glu Ile Ser Tyr Arg Glu Glu
 225 230 235 240
 Leu Leu Gln Gln Leu Met Lys Cys Asp Pro Pro Pro His Pro Met Gln
 245 250 255
 Gln Leu Leu Pro Glu Lys Leu Leu Met Glu Asn Arg Ala Lys Gly Thr
 260 265 270
 Pro Gln Leu Thr Ala Asn Gln Val Ala Val Ile Tyr Lys Leu Ile Trp
 275 280 285
 Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Ile
 290 295 300
 Thr Thr Glu Leu Glu Glu Glu Glu Asp Gln Glu His Glu Ala Asn Phe
 305 310 315 320
 Arg Tyr Ile Thr Glu Val Thr Ile Leu Thr Val Gln Leu Ile Val Glu
 325 330 335
 Phe Ala Lys Gly Leu Pro Ala Phe Ile Lys Ile Pro Gln Glu Asp Gln
 340 345 350
 Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met
 355 360 365
 Ala Arg Arg Tyr Asp His Asp Ser Asp Ser Ile Leu Phe Ala Asn Asn
 370 375 380
 Thr Ala Tyr Thr Lys Gln Thr Tyr Gln Leu Ala Gly Met Glu Glu Thr
 385 390 395 400
 Ile Asp Asp Leu Leu His Phe Cys Arg Gln Met Tyr Ala Leu Ser Ile
 405 410 415
 Asp Asn Val Glu Thr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp
 420 425 430
 Arg Pro Gly Leu Glu Lys Ala Glu Met Val Asp Ile Ile Gln Ser Tyr
 435 440 445
 Tyr Thr Glu Thr Leu Lys Val Tyr Ile Val Arg Asp His Gly Gly Glu
 450 455 460
 Ser Arg Cys Ser Val Gln Phe Ala Lys Leu Leu Gly Ile Leu Thr Glu
 465 470 475 480
 Leu Arg Thr Met Gly Asn Leu Asn Ser Glu Met Cys Phe Ser Leu Lys
 485 490 495
 Leu Arg Asn Arg Lys Leu Pro Arg Phe Leu Glu Glu Val Trp Asp Val
 500 505 510
 Gly Asp Val Asn Asn Gln Thr Thr Ala Thr Thr Asn Thr Glu Asn Ile
 515 520 525

Val Arg Glu Arg Ile Asn Arg Asn
 530 535

<210> 10
 <211> 606
 <212> PRT
 <213> Bombyx mori

<400> 10

Met Arg Val Glu Asn Val Asp Asn Val Ser Phe Ala Leu Asn Gly Arg
 1 5 10 15
 Ala Asp Glu Trp Cys Met Ser Val Glu Thr Arg Leu Asp Ser Leu Val
 20 25 30
 Arg Glu Lys Ser Glu Val Lys Ala Tyr Val Gly Gly Cys Pro Ser Val
 35 40 45
 Ile Thr Asp Ala Gly Ala Tyr Asp Ala Leu Phe Asp Met Arg Arg Arg
 50 55 60
 Trp Ser Asn Asn Gly Gly Phe Pro Leu Arg Met Leu Glu Glu Ser Ser
 65 70 75 80
 Ser Glu Val Thr Ser Ser Ser Ala Leu Gly Leu Pro Pro Ala Met Val
 85 90 95
 Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly Ala Leu Glu Leu
 100 105 110
 Trp Ser Tyr Asp Asp Gly Ile Thr Tyr Asn Thr Ala Gln Ser Leu Leu
 115 120 125
 Gly Ala Cys Asn Met Gln Gln Gln Gln Leu Gln Pro Gln Gln Pro His
 130 135 140
 Pro Ala Pro Pro Thr Leu Pro Thr Met Pro Leu Pro Met Pro Pro Thr
 145 150 155 160
 Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly Arg Glu Glu Leu
 165 170 175
 Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Ala Asp Ala Asp Ala Arg
 180 185 190
 Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu Glu Leu Cys Leu
 195 200 205
 Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys
 210 215 220
 Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val
 225 230 235 240
 Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp Met Tyr Met Arg
 245 250 255
 Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met
 260 265 270
 Arg Pro Glu Cys Val Ile Gln Glu Pro Ser Lys Asn Lys Asp Arg Gln
 275 280 285
 Arg Gln Lys Lys Asp Lys Gly Ile Leu Leu Pro Val Ser Thr Thr Thr
 290 295 300

Val Glu Asp His Met Pro Pro Ile Met Gln Cys Asp Pro Pro Pro Pro
 305 310 315 320
 Glu Ala Ala Arg Ile His Glu Val Val Pro Arg Tyr Leu Ser Glu Lys
 325 330 335
 Leu Met Glu Gln Asn Arg Gln Lys Asn Ile Pro Pro Leu Ser Ala Asn
 340 345 350
 Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr Gln Glu Gly Tyr Glu
 355 360 365
 Gln Pro Ser Asp Glu Asp Leu Lys Arg Val Thr Gln Thr Trp Gln Ser
 370 375 380
 Asp Glu Glu Asp Glu Glu Ser Asp Leu Pro Phe Arg Gln Ile Thr Glu
 385 390 395 400
 Met Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu
 405 410 415
 Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp Gln Ile Thr Leu Leu Lys
 420 425 430
 Ala Ser Ser Ser Glu Val Met Met Leu Arg Val Ala Arg Arg Tyr Asp
 435 440 445
 Ala Ala Ser Asp Ser Val Leu Phe Ala Asn Asn Lys Ala Tyr Thr Arg
 450 455 460
 Asp Asn Tyr Arg Gln Gly Gly Met Ala Tyr Val Ile Glu Asp Leu Leu
 465 470 475 480
 His Phe Cys Arg Cys Met Phe Ala Met Gly Met Asp Asn Val His Phe
 485 490 495
 Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu
 500 505 510
 Gln Pro Ser Leu Val Glu Glu Ile Gln Arg Tyr Tyr Leu Asn Thr Leu
 515 520 525
 Arg Ile Tyr Ile Ile Asn Gln Asn Ser Ala Ser Ser Arg Cys Ala Val
 530 535 540
 Ile Tyr Gly Arg Ile Leu Ser Val Leu Thr Glu Leu Arg Thr Leu Gly
 545 550 555 560
 Thr Gln Asn Ser Asn Met Cys Ile Ser Leu Lys Leu Lys Asn Arg Lys
 565 570 575
 Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp Val Ala Glu Val Ala Arg
 580 585 590
 Arg His Pro Thr Val Leu Pro Pro Thr Asn Pro Val Val Leu
 595 600 605
 <210> 11
 <211> 556
 <212> PRT
 <213> Manduca sexta
 <400> 11
 Met Arg Arg Arg Trp Ser Asn Asn Gly Cys Phe Pro Leu Arg Met Phe
 1 5 10 15

Glu Glu Ser Ser Ser Glu Val Thr Ser Ser Ser Ala Phe Gly Met Pro
 20 25 30
 Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly
 35 40 45
 Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala
 50 55 60
 Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln Gln
 65 70 75 80
 Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro
 85 90 95
 Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly
 100 105 110
 Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp
 115 120 125
 Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
 130 135 140
 Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
 145 150 155 160
 Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
 165 170 175
 Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp
 180 185 190
 Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu
 195 200 205
 Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Ser Thr Cys Lys
 210 215 220
 Asn Lys Arg Arg Glu Lys Glu Ala Gln Arg Glu Lys Asp Lys Leu Pro
 225 230 235 240
 Val Ser Thr Thr Thr Val Asp Asp His Met Pro Ala Ile Met Gln Cys
 245 250 255
 Asp Pro Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg
 260 265 270
 Phe Leu Thr Glu Lys Leu Met Glu Gln Asn Arg Leu Lys Asn Val Thr
 275 280 285
 Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Met Tyr
 290 295 300
 Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr
 305 310 315 320
 Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Glu Thr Asp Met Pro
 325 330 335
 Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val
 340 345 350
 Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp
 355 360 365

Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg
 370 375 380
 Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn
 385 390 395 400
 Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr
 405 410 415
 Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser
 420 425 430
 Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser
 435 440 445
 Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg
 450 455 460
 Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala
 465 470 475 480
 Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr
 485 490 495
 Glu Leu Arg Thr Leu Gly Thr Gln Asn Ser Asn Met Cys Ile Ser Leu
 500 505 510
 Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp
 515 520 525
 Val Ala Glu Val Ser Thr Thr Gln Pro Thr Pro Gly Val Ala Ala Gln
 530 535 540
 Val Thr Pro Ile Val Val Asp Asn Pro Ala Ala Leu
 545 550 555

<210> 12
 <211> 675
 <212> PRT
 <213> Aedes aegypti

<400> 12

Met Met Lys Arg Arg Trp Ser Asn Asn Gly Gly Phe Thr Ala Leu Arg
 1 5 10 15
 Met Leu Asp Asp Ser Ser Ser Glu Val Thr Ser Ser Ser Ala Ala Leu
 20 25 30
 Gly Met Thr Met Ser Pro Asn Ser Leu Gly Ser Pro Asn Tyr Asp Glu
 35 40 45
 Leu Glu Leu Trp Ser Ser Tyr Glu Asp Asn Ala Tyr Asn Gly His Ser
 50 55 60
 Val Leu Ser Asn Gly Asn Asn Asn Leu Gly Gly Cys Gly Ala Ala Asn
 65 70 75 80
 Asn Leu Leu Met Asn Gly Ile Val Gly Asn Asn Asn Leu Asn Gly Met
 85 90 95
 Met Asn Met Ala Ser Gln Ala Val Gln Ala Asn Ala Asn Ser Ile Gln
 100 105 110
 His Ile Val Gly Asn Leu Ile Asn Gly Val Asn Pro Asn Gln Thr Leu
 115 120 125

Ile Pro Pro Leu Pro Ser Ile Ile Gln Asn Thr Leu Met Asn Thr Pro
 130 135 140
 Arg Ser Glu Ser Val Asn Ser Ile Ser Ser Gly Arg Glu Asp Leu Ser
 145 150 155 160
 Pro Ser Ser Ser Leu Asn Gly Tyr Thr Asp Gly Ser Asp Ala Lys Lys
 165 170 175
 Gln Lys Lys Gly Pro Thr Pro Arg Gln Gln Glu Glu Leu Cys Leu Val
 180 185 190
 Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu
 195 200 205
 Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val Tyr
 210 215 220
 Cys Cys Lys Phe Gly His Ala Cys Glu Met Asp Met Tyr Met Arg Arg
 225 230 235 240
 Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg
 245 250 255
 Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Ile Lys Arg Lys Glu
 260 265 270
 Lys Lys Ala Gln Lys Glu Lys Asp Lys Val Gln Thr Asn Ala Thr Val
 275 280 285
 Ser Thr Thr Asn Ser Thr Tyr Arg Ser Glu Ile Leu Pro Ile Leu Met
 290 295 300
 Lys Cys Asp Pro Pro Pro His Gln Ala Ile Pro Leu Leu Pro Glu Lys
 305 310 315 320
 Leu Leu Gln Glu Asn Arg Leu Arg Asn Ile Pro Leu Leu Thr Ala Asn
 325 330 335
 Gln Met Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu
 340 345 350
 Gln Pro Ser Glu Glu Asp Leu Lys Arg Ile Met Ile Gly Ser Pro Asn
 355 360 365
 Glu Glu Glu Asp Gln His Asp Val His Phe Arg His Ile Thr Glu Ile
 370 375 380
 Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro
 385 390 395 400
 Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala
 405 410 415
 Cys Ser Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp Ala
 420 425 430
 Ala Thr Asp Ser Ile Leu Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp
 435 440 445
 Ser Tyr Arg Met Ala Gly Met Ala Asp Thr Ile Glu Asp Leu Leu His
 450 455 460
 Phe Cys Arg Gln Met Phe Ser Leu Thr Val Asp Asn Val Glu Tyr Ala
 465 470 475 480
 Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Gln

485 490 495
 Ala Glu Leu Val Glu His Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg
 500 505 510
 Ile Tyr Ile Leu Asn Arg His Ala Gly Asp Pro Lys Cys Ser Val Ile
 515 520 525
 Phe Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn
 530 535 540
 Gln Asn Ser Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu
 545 550 555 560
 Pro Arg Phe Leu Glu Glu Ile Trp Asp Val Gln Asp Ile Pro Pro Ser
 565 570 575
 Met Gln Ala Gln Met His Ser His Gly Thr Gln Ser Ser Ser Ser Ser
 580 585 590
 Ser Ser Ser Ser Ser Ser Ser Ser Asn Gly Ser Ser Asn Gly Asn Ser
 595 600 605
 Ser Ser Asn Ser Asn Ser Ser Gln His Gly Pro His Pro His Pro His
 610 615 620
 Gly Gln Gln Leu Thr Pro Asn Gln Gln Gln His Gln Gln Gln His Ser
 625 630 635 640
 Gln Leu Gln Gln Val His Ala Asn Gly Ser Gly Ser Gly Gly Gly Ser
 645 650 655
 Asn Asn Asn Ser Ser Ser Gly Gly Val Val Pro Gly Leu Gly Met Leu
 660 665 670
 Asp Gln Val
 675
 <210> 13
 <211> 319
 <212> PRT
 <213> *Heliothis virescens*
 <400> 13
 Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Lys
 1 5 10 15
 Glu Lys Lys Ala Gln Arg Glu Lys Asp Lys Leu Pro Val Ser Thr Thr
 20 25 30
 Thr Val Asp Asp His Met Pro Pro Ile Met Gln Cys Asp Pro Pro Pro
 35 40 45
 Pro Glu Ala Ala Arg Ile Leu Glu Cys Val Gln His Glu Val Val Pro
 50 55 60
 Arg Phe Leu Asn Glu Lys Leu Met Glu Gln Asn Arg Leu Lys Asn Val
 65 70 75 80
 Pro Pro Leu Thr Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp
 85 90 95
 Tyr Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val
 100 105 110
 Thr Gln Ser Asp Glu Asp Asp Glu Asp Ser Asp Met Pro Phe Arg Gln

115					120					125					
Ile	Thr	Glu	Met	Thr	Ile	Leu	Thr	Val	Gln	Leu	Ile	Val	Glu	Phe	Ala
130					135					140					
Lys	Gly	Leu	Pro	Gly	Phe	Ala	Lys	Ile	Ser	Gln	Ser	Asp	Gln	Ile	Thr
145					150					155					160
Leu	Leu	Lys	Ala	Cys	Ser	Ser	Glu	Val	Met	Met	Leu	Arg	Val	Ala	Arg
				165					170					175	
Arg	Tyr	Asp	Ala	Ala	Thr	Asp	Ser	Val	Leu	Phe	Ala	Asn	Asn	Gln	Ala
			180					185					190		
Tyr	Thr	Arg	Asp	Asn	Tyr	Arg	Lys	Ala	Gly	Met	Ala	Tyr	Val	Ile	Glu
		195					200					205			
Asp	Leu	Leu	His	Phe	Cys	Arg	Cys	Met	Tyr	Ser	Met	Met	Met	Asp	Asn
	210					215					220				
Val	His	Tyr	Ala	Leu	Leu	Thr	Ala	Ile	Val	Ile	Phe	Ser	Asp	Arg	Pro
225					230					235					240
Gly	Leu	Glu	Gln	Pro	Leu	Leu	Val	Glu	Glu	Ile	Gln	Arg	Tyr	Tyr	Leu
				245					250					255	
Asn	Thr	Leu	Arg	Val	Tyr	Ile	Leu	Asn	Gln	Asn	Ser	Ala	Ser	Pro	Arg
			260					265					270		
Gly	Ala	Val	Ile	Phe	Gly	Glu	Ile	Leu	Gly	Ile	Leu	Thr	Glu	Ile	Arg
		275					280					285			
Thr	Leu	Gly	Met	Gln	Asn	Ser	Asn	Met	Cys	Ile	Ser	Leu	Lys	Leu	Lys
	290					295					300				
Lys	Arg	Lys	Leu	Pro	Pro	Phe	Leu	Glu	Glu	Ile	Asp	Trp	Asp	Val	
305					310					315					

<210> 14
 <211> 8
 <212> PRT
 <213> Artificial

<220>
 <223> Conserved motif within DNA binding domain of RAR and THR receptors

<400> 14

Cys Glu Gly Cys Lys Gly Phe Phe
 1 5

<210> 15
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> Degenerate sense oligonucleotide

<220>
 <221> misc_feature
 <222> (1)..(23)
 <223> y=c or t

<220>
 <221> misc_feature

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<222> (1)..(23)
<223> r=g or a

<220>
<221> misc_feature
<222> (1)..(23)
<223> n=inosine

<400> 15
tgygarggnt gyaargantt ytt
23

<210> 16
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Peptide sequence corresponding to conserved motif used for
degenerate antisense oligonucleotide

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X=E or S

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X=L or R

<400> 16
Cys Gln Xaa Cys Arg Xaa Lys Lys
1 5

<210> 17
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Degenerate oligo ZnFA3'

<220>
<221> misc_feature
<222> (1)..(23)
<223> r=g or a

<220>
<221> misc_feature
<222> (1)..(23)
<223> y=c or t

<220>
<221> misc_feature
<222> (1)..(23)
<223> n=inosine

<400> 17
ttyttnagnc grcaytcytg rca
23

<210> 18
<211> 23
<212> DNA
<213> Artificial

<220>

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<223> Degenerate oligo ZnFB3'

<220>

<221> misc_feature

<222> (1)..(23)

<223> r=g or a

<220>

<221> misc_feature

<222> (1)..(23)

<223> y=c or t

<220>

<221> misc_feature

<222> (1)..(23)

<223> n=inosine

<400> 18

ttyttnaanc grcaytcytcg rca

23

<210> 19

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Degenerate oligo ZnFC3'

<220>

<221> misc_feature

<222> (1)..(23)

<223> r=g or a

<220>

<221> misc_feature

<222> (1)..(23)

<223> y=c or t

<220>

<221> misc_feature

<222> (1)..(23)

<223> n=inosine

<400> 19

ttyttnagnc trcaytcytcg rca

23

<210> 20

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Degenerate oligo ZnFD3'

<220>

<221> misc_feature

<222> (1)..(23)

<223> r=g or a

<220>

<221> misc_feature

<222> (1)..(23)

<223> y=c or t

<220>

<221> misc_feature

<222> (1)..(23)

<223> n=inosine

<400> 20
ttypnaanc trcaytcytcg rca 23

<210> 21
<211> 39
<212> DNA
<213> Artificial

<220>
<223> PCR sense oligonucleotide used to isolate the full 5' end
sequence of *H. virescens* gene

<400> 21
aattaagctt ccaccatgcc gttaccaatg ccaccgaca 39

<210> 22
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Antisense primer used to isolate correct 5' end of *H. virescens*
gene

<400> 22
cttcaaccga cactcctgac 20

<210> 23
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Sense primer used to isolate correct 5' end of *H. virescens* gene

<400> 23
cagctccagg ccgccgatct cg 22

<210> 24
<211> 48
<212> DNA
<213> Artificial

<220>
<223> Anchor primer used to isolate correct 5' end of *H. virescens* gene

<220>
<221> misc_feature
<222> (1)..(48)
<223> n=inosine

<400> 24
cuacuacuac uaggccacgc gtcgactagt acggggnnggg nngggngng 48

<210> 25
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Universal amplification primer used to isolate correct 5' end of
H. virescens gene

<400> 25
caucaucauc auggccacgc gtcgactagt ac 32

<210> 26
 <211> 27
 <212> DNA
 <213> Artificial

 <220>
 <223> Primer used to isolate correct 5' end of *H. virescens* gene

 <400> 26
 acgtcacctc agacgagctc tccattc 27

 <210> 27
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <223> Primer used to confirm correct 5' end of *H. virescens* gene

 <400> 27
 cgctggtata acaacggacc attc 24

 <210> 28
 <211> 48
 <212> DNA
 <213> Artificial

 <220>
 <223> Primer used to incorporate HindIII site, Kozak consensus
 sequence, and Met-Arg-Arg into third effector construct

 <400> 28
 attaagcttg cgcctatgcg ccgacgctgg tataacaacg gaccattc 48

 <210> 29
 <211> 39
 <212> DNA
 <213> Artificial

 <220>
 <223> Sense oligo used to introduce HindIII site and Kozak consensus
 sequence into fourth effector construct

 <400> 29
 attaagcttg cgcctatgtc cctcggcgct cgtggatac 39

 <210> 30
 <211> 137
 <212> DNA
 <213> Artificial

 <220>
 <223> Oligo that is complementary to SEQ ID NO: 31, which when annealed
 encode tandem repeats of the ecdysone response element flanked by
 SpeI and ClaI sites

 <400> 30
 ctagtagaca agggttcaat gcacttgctc aataagctta gacaagggtt caatgcactt 60

 gtccaatgaa ttcagacaag ggttcaatgc acttggtccaa tctgcagaga caagggttca 120

 atgcacttgt ccaatat 137

 <210> 31
 <211> 135
 <212> DNA

<213> Artificial

<220>

<223> Oligo that is complementary to SEQ ID NO: 30, which when annealed encode tandem repeats of the ecdysone response element flanked by SpeI and ClaI sites

<400> 31
cgatattgga caagtgcatt gaacccttgt ctctgcagat tggacaagtg cattgaaccc 60
ttgtctgaat tcattggaca agtgcattga acccttgtct aagcttattg gacaagtgca 120
ttgaaccctt gtcta 135

<210> 32
<211> 38
<212> DNA
<213> Artificial

<220>

<223> PCR primer used to incorporate an EcoRI site and a Kozak consensus sequence into an expression construct

<400> 32
attgaattcc accatggact ccaaagaatc attaactc 38

<210> 33
<211> 42
<212> DNA
<213> Artificial

<220>

<223> 3' primer used to incorporate an XhoI site in frame with the reading frame at amino acid 500 of the human glucocorticoid receptor

<400> 33
gagactcctg tagtggcctc gagcattcct tttatttttt tc 42

<210> 34
<211> 31
<212> DNA
<213> Artificial

<220>

<223> 5' primer incorporating an XhoI site at amino acid 500 of the human glucocorticoid receptor

<400> 34
attctcgaga ttcagcaggc cactacagga g 31

<210> 35
<211> 32
<212> DNA
<213> Artificial

<220>

<223> 3' primer used to incorporate an EcoRI site 400 bp downstream of the human glucocorticoid receptor ORF

<400> 35
attgaattca atgctatcgt aactatacag gg 32

<210> 36
<211> 35
<212> DNA
<213> Artificial

<220>
 <223> 5' oligo containing a SalI site at the beginning of the hinge region of the Drosophila ecdysone receptor cDNA

<400> 36
 attgtcgaca acggccggaa tggctcgtcc cggag 35

<210> 37
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <223> 3' oligo used to incorporate a BamHI site adjacent to the stop codon of the Drosophila ecdysone receptor cDNA

<400> 37
 tcgggctttg ttaggatcct aagccgtggt cgaatgctcc gacttaac 48

<210> 38
 <211> 35
 <212> DNA
 <213> Artificial

<220>
 <223> Oligo used to incorporate a SalI site at the DNAbinding/hinge domain junction of hte Heliothis ecdysone receptor cDNA

<400> 38
 attgtcgaca aaggcccgag tgcgtggtgc cggag 35

<210> 39
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Primer used to achieve PCR-mediated mutagenesis adding a SalI site downstream of the DNA binding/hinge domain junction

<400> 39
 tcacattgca tgatgggagg catg 24

<210> 40
 <211> 82
 <212> DNA
 <213> Artificial

<220>
 <223> Oligo that anneals to SEQ ID NO: 41 to produce a double-stranded DNA encoding six copies of hte glucocorticoid response element flanked by HindIII and SalI sites

<400> 40
 agcttcgact gtacaggatg ttctagctac tcgagtagct agaacatcct gtacagtcga 60
 gtagctagaa catcctgtac ag 82

<210> 41
 <211> 82
 <212> DNA
 <213> Artificial

<220>
 <223> Oligo that anneals to SEQ ID NO: 40 to produce a double-stranded DNA encoding six copies of hte glucocorticoid response element

flanked by HindIII and SalI sites

```

<400> 41
tcgactgtac aggatgttct agctactcga ctgtacagga tgttctagct actcgagtcg      60
ctagaacatc ctgtacagtc ga                                              82

<210> 42
<211> 78
<212> DNA
<213> Artificial

<220>
<223> Oligo that anneals to SEQ ID NO: 43 to produce a double-stranded
      DNA encoding six copies of hte glucocorticoid response element
      flanked by SalI and BanHI sites

<400> 42
tcgactagct agaacatcct gtacagtcga gtagctagaa catcctgtac agtcgagtag      60
ctagaacatc ctgtacag                                              78

<210> 43
<211> 78
<212> DNA
<213> Artificial

<220>
<223> Oligo that anneals to SEQ ID NO: 42 to produce a double-stranded
      DNA encoding six copies of hte glucocorticoid response element
      flanked by SalI and BanHI sites

<400> 43
gatcctgtac aggatgttct agctactcga ctgtacagga tgttctagct actcgactgt      60
acaggatggt ctagctag                                              78

<210> 44
<211> 104
<212> DNA
<213> Artificial

<220>
<223> 5' oligo used with SEQ ID NO: 45 to incorporate 4 copies of the
      glucocorticoid response element flanked by SpeI and AflIII sites
      into pSWBGAL

<400> 44
ctagttgtac aggatgttct agctactcga gtagctagaa catcctgtac agtcgagtag      60
ctagaacatc ctgtacagtc gagtagctag aacatcctgt acac                    104

<210> 45
<211> 104
<212> DNA
<213> Artificial

<220>
<223> 3' oligo used with SEQ ID NO: 44 to incorporate 4 copies of the
      glucocorticoid response element flanked by SpeI and AflIII sites
      into pSWBGAL

<400> 45
ttaagtgtac aggatgttct agctactcga ctgtacagga tgttctagct actcgactgt      60
acaggatggt ctagctactc gagtagctag aacatcctgt acaa                    104

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<210> 46
 <211> 15
 <212> DNA
 <213> Artificial

 <220>
 <223> Oligo that in conjunction with SEQ ID NO: 47 creates an ApaI/NotI linker

 <400> 46
 cattggatcc ttagc 15

 <210> 47
 <211> 23
 <212> DNA
 <213> Artificial

 <220>
 <223> Oligo that in conjunction with SEQ ID NO: 46 creates an ApaI/NotI linker

 <400> 47
 ggccgctaag gatccaatgg gcc 23

 <210> 48
 <211> 32
 <212> DNA
 <213> Artificial

 <220>
 <223> 5' oligo used to introduce an NcoI site into amino acid 259 of the Heliothis ecdysone receptor ORF

 <400> 48
 aattccatgg tacgacgaca gtagacgac ac 32

 <210> 49
 <211> 29
 <212> DNA
 <213> Artificial

 <220>
 <223> 3' oligo used to introduce an XbaI site flanking amino acid 571 of the Heliothis ecdysone receptor ORF

 <400> 49
 ctgaggtcta gagacggtgg cgggcggcc 29

 <210> 50
 <211> 31
 <212> DNA
 <213> Artificial

 <220>
 <223> 5' oligo used to introduce Kozak consensus sequences, a methionine start codon, and an coding sequence up to amino acid 152 of the glucocorticoid receptor, with an upstream EcoRI site

 <400> 50
 atatgaattc caccatggac tccaaagaat c 31

 <210> 51
 <211> 36
 <212> DNA
 <213> Artificial

 <220>

<223> 3' oligo used to introduce Kozak consensus sequences, a methionine start codon, and an coding sequence up to amino acid 152 of the glucocorticoid receptor, and a downstream NheI site

<400> 51
 atatgctagc tgtgggggca gcagacacag cagtgg 36

<210> 52
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> 5' primer that incorporates an NheI site into the codon for amino acid 406 of the glucocorticoid receptor

<400> 52
 atatgctagc tccagctcct caacagcaac aac 33

<210> 53
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> 3' oligo that incorporates an XhoI site at amino acid 500 of the glucocorticoid receptor

<400> 53
 atatctcgag caattccttt tatttttttc 30

<210> 54
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> 5' oligo used to amplify amino acids 411-490 of the herpes simplex VP16 protein, incorporating flanking SpeI sites

<400> 54
 attactagtt ctgcggcccc cccgaccgat 30

<210> 55
 <211> 31
 <212> DNA
 <213> Artificial

<220>
 <223> 3' oligo used to amplify amino acids 411-490 of the herpes simplex VP16 protein, incorporating flanking SpeI sites

<400> 55
 aattactagt cccaccgtac tcgtcaattc c 31

<210> 56
 <211> 32
 <212> DNA
 <213> Artificial

<220>
 <223> 5' degenerate oligo used to isolate ecdysone ligand binding domains from other lepidopteran species

<220>
 <221> misc_feature
 <222> (1)..(32)

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<223> n=inosine

<220>
<221> misc_feature
<222> (1)..(32)
<223> w=t or a

<220>
<221> misc_feature
<222> (1)..(32)
<223> k=g or t

<400> 56
attgctcgag aaagncnnga gwgcktnngtn cc 32

<210> 57
<211> 32
<212> DNA
<213> Artificial

<220>
<223> 5' degenerate oligo used to isolate ecdysone ligand binding
domains from other lepidopteran species

<220>
<221> misc_feature
<222> (1)..(32)
<223> n=inosine

<220>
<221> misc_feature
<222> (1)..(32)
<223> w=t or a

<220>
<221> misc_feature
<222> (1)..(32)
<223> s=g or c

<400> 57
attgctcgag aacgncnnga gwgtsnngtn cc 32

<210> 58
<211> 33
<212> DNA
<213> Artificial

<220>
<223> 3' degenerate oligo used to isolate ecdysone ligand binding
domains from other lepidopteran species

<220>
<221> misc_feature
<222> (1)..(33)
<223> n=inosine

<220>
<221> misc_feature
<222> (1)..(33)
<223> w=t or a

<220>
<221> misc_feature
<222> (1)..(33)
<223> y=t or c

<400> 58

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ttactcgagn acgwcccana tctctycnag gaa 33

<210> 59
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> 3' degenerate oligo used to isolate ecdysone ligand binding domains from other lepidopteran species

<220>
 <221> misc_feature
 <222> (1)..(33)
 <223> n=inosine

<220>
 <221> misc_feature
 <222> (1)..(33)
 <223> w=t or a

<220>
 <221> misc_feature
 <222> (1)..(33)
 <223> y=c or t

<400> 59
 ttactcgagn acgwcccana tctcctynaa gaa 33